



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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MCKEOWN, MICHAEL B.
ORO, ANTHONY E.
SEGRAVES, WILLIAM A.
YAO, TSO-PANG
- (ii) TITLE OF INVENTION: MULTIMERIC FORMS OF MEMBERS OF THE
STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH THE
ULTRASPIRACLE RECEPTOR
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
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 - (B) STREET: 444 South Flower Street, Suite 2000
 - (C) CITY: Los Angeles
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/907,908
 - (B) FILING DATE: 02-JUL-1992
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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 - (C) REFERENCE/DOCKET NUMBER: P41 9321
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 163..1701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGACACGGTG GCGTTGGCAA AGTGAAACCC CAACAGAGAG GCGAAAGCGA GCCAAGACAC 60
ACCACATACA CACGAAGAGA ACGAGCAAGA AGAAACCGGT AGGCGGAGGA GGCGCTGCCC 120

CCAGTTCCTC CAATATACCC AGCACCACAT CACAAGCCCA GG ATG GAC AAC TGC Met Asp Asn Cys 1															174	
GAC Asp 5	CAG Gln	GAC Asp	GCC Ala	AGC Ser	TTT Phe 10	CGG Arg	CTG Leu	AGC Ser	CAC His	ATC Ile 15	AAG Lys	GAG Glu	GAG Glu	GTC Val	AAG Lys 20	222
CCG Pro	GAC Asp	ATC Ile	TCG Ser	CAG Gln 25	CTG Leu	AAC Asn	GAC Asp	AGC Ser	AAC Asn 30	AAC Asn	AGC Ser	AGG Ser	TTT Phe	TCG Ser 35	CCC Pro	270
AAG Lys	GCC Ala	GAG Glu	AGT Ser 40	CCC Pro	GTG Val	CCC Pro	TTC Phe	ATG Met 45	CAG Gln	GCC Ala	ATG Met	TCC Ser	ATG Met 50	GTC Val	CAC His	318
GTG Val	CTG Leu	CCC Pro 55	GGC Gly	TCC Ser	AAC Asn	TCC Ser	GCC Ala 60	AGC Ser	TCC Ser	AAC Asn	AAC Asn 65	AAC Asn	AGC Ser	GCT Ala	GGA Gly	366
GAT Asp 70	GCC Ala	CAA Gln	ATG Met	GCG Ala	CAG Gln 75	GCG Ala	CCC Pro	AAT Asn	TCG Ser	GCT Ala	GGA Gly 80	GGC Gly	TCT Ser	GCC Ala	GCC Ala	414
GCT Ala 85	GCA Ala	GTC Val	CAG Gln	CAG Gln 90	CAG Gln	TAT Tyr	CCG Pro	CCT Pro	AAC Asn	CAT His 95	CCG Pro	CTG Leu	AGC Ser	GGC Gly	AGC Ser 100	462
AAG Lys	CAC His	CTC Leu	TGC Cys 105	TCT Ser	ATT Ile	TGC Cys	GGG Gly	GAT Asp 110	CGG Arg	GCC Ala	AGT Ser	GGC Gly	AAG Lys 115	CAC His	TAC Tyr	510
GGC Gly	GTG Val	TAC Tyr	AGC Ser 120	TGT Cys	GAG Glu	GGC Gly	TGC Cys	AAG Lys 125	GGC Gly	TTC Phe	TTT Phe	AAA Lys 130	CGC Arg	ACA Thr	GTG Val	558
CGC Arg	AAG Lys 135	GAT Asp	CTC Leu	ACA Thr	TAC Tyr	GCT Ala	TGC Cys 140	AGG Arg	GAG Glu	AAC Asn	CGC Arg 145	AAC Asn	TGC Cys	ATC Ile	ATA Ile	606
GAC Asp 150	AAG Lys	CGG Arg	CAG Gln	AGG Arg	AAC Asn 155	CGC Arg	TGC Cys	CAG Gln	TAC Tyr	TGC Cys 160	CGC Arg	TAC Tyr	CAG Gln	AAG Lys	TGC Cys	654
CTA Leu 165	ACC Thr	TGC Cys	GGC Gly	ATG Met 170	AAG Lys	CGC Arg	GAA Glu	GCG Ala	GTC Val	CAG Gln 175	GAG Glu	GAG Glu	CGT Arg	CAA Gln	CGC Arg 180	702
GGC Gly	GCC Ala	CGC Arg	AAT Asn 185	GCG Ala	GCG Ala	GGT Gly	AGG Arg	CTC Leu	AGC Ser 190	GCC Ala	AGC Ser	GGA Gly	GGC Gly	GGC Gly	AGT Ser 195	750
AGC Ser	GGT Gly	CCA Pro	GGT Gly 200	TCG Ser	GTA Val	GGC Gly	GGA Gly	TCC Ser 205	AGC Ser	TCT Ser	CAA Gln	GGC Gly 210	GGA Gly	GGA Gly	GGA Gly	798
GGA Gly	GGC Gly	GGC Gly 215	GTT Val	TCT Ser	GGC Gly	GGA Gly	ATG Met 220	GGC Gly	AGC Ser	GGC Gly	AAC Asn 225	GGT Gly 225	TCT Ser	GAT Asp	GAC Asp	846
TTC Phe 230	ATG Met	ACC Thr	AAT Asn	AGC Ser	GTG Val	TCC Ser 235	AGG Arg	GAT Asp	TTC Phe	TCG Ser 240	ATC Ile	GAG Glu	CGC Arg	ATC Ile	ATA Ile	894
GAG Glu 245	GCC Ala	GAG Glu	CAG Gln	CGA Arg 250	GCG Ala	GAG Glu	ACC Thr	CAA Gln	TGC Cys	GGC Gly 255	GAT Asp	CGT Arg	GCA Ala	CTG Leu 260	ACG Thr	942

TTC	CTG	CGC	GTT	GGT	CCC	TAT	TCC	ACA	GTC	CAG	CCG	GAC	TAC	AAG	GGT	990
Phe	Leu	Arg	Val	Gly	Pro	Tyr	Ser	Thr	Val	Gln	Pro	Asp	Tyr	Lys	Gly	
				265					270					275		
GCC	GTG	TCG	GCC	CTG	TGC	CAA	GTG	GTC	AAC	AAA	CAG	CTC	TTC	CAG	ATG	1038
Ala	Val	Ser	Ala	Leu	Cys	Gln	Val	Val	Asn	Lys	Gln	Leu	Phe	Gln	Met	
			280					285					290			
GTC	GAA	TAC	GCG	CGC	ATG	ATG	CCG	CAC	TTT	GCC	CAG	GTG	CCG	CTG	GAC	1086
Val	Glu	Tyr	Ala	Arg	Met	Met	Pro	His	Phe	Ala	Gln	Val	Pro	Leu	Asp	
		295					300					305				
GAC	CAG	GTG	ATT	CTG	CTG	AAA	GCC	GCT	TGG	ATC	GAG	CTG	CTC	ATT	GCG	1134
Asp	Gln	Val	Ile	Leu	Leu	Lys	Ala	Ala	Trp	Ile	Glu	Leu	Leu	Ile	Ala	
	310					315					320					
AAC	GTG	GCC	TGG	TGC	AGC	ATC	GTT	TCG	CTG	GAT	GAC	GGC	GGT	GCC	GGC	1182
Asn	Val	Ala	Trp	Cys	Ser	Ile	Val	Ser	Leu	Asp	Asp	Gly	Gly	Ala	Gly	
	325				330					335					340	
GGC	GGG	GGC	GGT	GGA	CTA	GGC	CAC	GAT	GGC	TCC	TTT	GAG	CGA	CGA	TCA	1230
Gly	Gly	Gly	Gly	Gly	Leu	Gly	His	Asp	Gly	Ser	Phe	Glu	Arg	Arg	Ser	
				345					350					355		
CCG	GGC	CTT	CAG	CCC	CAG	CAG	CTG	TTC	CTC	AAC	CAG	AGC	TTC	TCG	TAC	1278
Pro	Gly	Leu	Gln	Pro	Gln	Gln	Leu	Phe	Leu	Asn	Gln	Ser	Phe	Ser	Tyr	
			360					365					370			
CAT	CGC	AAC	AGT	GCG	ATC	AAA	GCC	GGT	GTG	TCA	GCC	ATC	TTC	GAC	CGC	1326
His	Arg	Asn	Ser	Ala	Ile	Lys	Ala	Gly	Val	Ser	Ala	Ile	Phe	Asp	Arg	
		375					380					385				
ATA	TTG	TCG	GAG	CTG	AGT	GTA	AAG	ATG	AAG	CGG	CTG	AAT	CTC	GAC	CGA	1374
Ile	Leu	Ser	Glu	Leu	Ser	Val	Lys	Met	Lys	Arg	Leu	Asn	Leu	Asp	Arg	
	390					395					400					
CGC	GAG	CTG	TCC	TGC	TTG	AAG	GCC	ATC	ATA	CTG	TAC	AAC	CCG	GAC	ATA	1422
Arg	Glu	Leu	Ser	Cys	Leu	Lys	Ala	Ile	Ile	Leu	Tyr	Asn	Pro	Asp	Ile	
	405				410					415					420	
CGC	GGG	ATC	AAG	AGC	CGG	GCG	GAG	ATC	GAG	ATG	TGC	CGC	GAG	AAG	GTG	1470
Arg	Gly	Ile	Lys	Ser	Arg	Ala	Glu	Ile	Glu	Met	Cys	Arg	Glu	Lys	Val	
				425					430					435		
TAC	GCT	TGC	CTG	GAC	GAG	CAC	TGC	CGC	CTG	GAA	CAT	CCG	GGC	GAC	GAT	1518
Tyr	Ala	Cys	Leu	Asp	Glu	His	Cys	Arg	Leu	Glu	His	Pro	Gly	Asp	Asp	
			440					445					450			
GGA	CGC	TTT	GCG	CAA	CTG	CTG	CTG	CGT	CTG	CGC	CGC	TTT	GCG	ATC	GAT	1566
Gly	Arg	Phe	Ala	Gln	Leu	Leu	Leu	Arg	Leu	Arg	Arg	Phe	Ala	Ile	Asp	
		455					460					465				

TATTACCTAA TATTATTATT ATTATTGATA TAGAAAATGT TTTCCTTAAG ATGAAGATTA 1891
 GCCTCCTCGA CGTTTATGTC CCAGTAAACG AAAACAAAC AAAATCCAAA ACTTGAAAAG 1951
 AACACAAAAC ACGAACGAGA AAATGCACAC AAGCAAAGTA AAAGTAAAAG TTAAACTAAA 2011
 GCTAAACGAG TAAAGATATT AAAATAACGG TTAAAATTAA TGCATAGTTA TGATCTACAG 2071
 ACGTATGTAA ACATACAAAT TCAGCATAAA TATATATGTC AGCAGGGGCA TATCTGCGGT 2131
 GCTGGCCCCG TTCTAAACCA ATTGTAATTA CTTTTTAACA TAAATTTACC CAAAACGTTA 2191
 TCAATTAGAT GCGAGATACA AAAATCACCG ACGAAAACCA ACAAATATA TCTATGTATA 2251
 AAAAATATAA GCTGCATAAC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 2304

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Asn Cys Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys
 1 5 10 15
 Glu Glu Val Lys Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser
 20 25 30
 Ser Phe Ser Pro Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met
 35 40 45
 Ser Met Val His Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn
 50 55 60
 Asn Ser Ala Gly Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly
 65 70 75 80
 Gly Ser Ala Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro
 85 90 95
 Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser
 100 105 110
 Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe
 115 120 125
 Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg
 130 135 140
 Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg
 145 150 155 160
 Tyr Gln Lys Cys Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu
 165 170 175
 Glu Arg Gln Arg Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser
 180 185 190
 Gly Gly Gly Ser Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln
 195 200 205

Gly Gly Gly Gly Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn
 210 215 220
 Gly Ser Asp Asp Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile
 225 230 235 240
 Glu Arg Ile Ile Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp
 245 250 255
 Arg Ala Leu Thr Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro
 260 265 270
 Asp Tyr Lys Gly Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln
 275 280 285
 Leu Phe Gln Met Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln
 290 295 300
 Val Pro Leu Asp Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu
 305 310 315 320
 Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp
 325 330 335
 Gly Gly Ala Gly Gly Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe
 340 345 350
 Glu Arg Arg Ser Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln
 355 360 365
 Ser Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala
 370 375 380
 Ile Phe Asp Arg Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu
 385 390 395 400
 Asn Leu Asp Arg Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr
 405 410 415
 Asn Pro Asp Ile Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys
 420 425 430
 Arg Glu Lys Val Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His
 435 440 445
 Pro Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Arg Arg
 450 455 460
 Phe Ala Ile Asp Gln Pro Glu Val Pro Gly Ser Pro Val Pro Leu Pro
 465 470 475 480
 His Tyr Gln Arg Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly
 485 490 495
 Gly Ala Ala Ala Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg
 500 505 510

Leu

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
 1 5 10 15
 Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 35 40 45
 Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
 50 55 60
 Lys Cys Xaa Xaa Xaa Gly Met
 65 70

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGTCAAGGA GGTCA

15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGTGAATGA GGACA

15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTGAACGG GGGCA

15

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCACGAG GTTCA

15

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGTCACAGG AGGTCA

16

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGTGACAGG AGGTCA

16

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGGTGACAGG AGGACA

16

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGTTAGGGG AGGACA

16

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGTCATTTC AGGTCC

16

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGTCACCAG GAGGTCA

17

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGGTGAACAG GAGGTCA

17

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTTCACCGA AAGTTCA

17

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTTCACCGA AAGTTCA

17

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTCAGTGA CAGGGCA

17

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGTCATTCA GAGTTCA

17

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAGCTTAAGG GTTCACCGAA AGTTCACTCA GCTT

34

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAGCTTAAGG GTTCACCGAA AGTTCACTCG CATAGCTT

38

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGCTTAAGG GTTCACCGAA AGTTCACTCG CATATATTAG CTT

43

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCTCGATGG ACAAGTGCAT TGAACCCTTG AGCTACCTGT TCACGTA ACT TGGGAACTTC 60

GA 62

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTGCGCCAC GGC GGCCGCC GGAGCTGTGC CTG 33

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGGGTATGC GCCTCGAGTG CGTCGTCCC 29

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGGACAAAGG TCA 13

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATTGGACAAG TGCATTGAAC CCTTGTCTCT

30

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCTGTGCA TTGAACGTGC TCGA

24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGAAGTGCA TTGAACCCGC TCGA

24

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAAAGGATCT TGACCCCAAT GAACTTCTTA

30